

Template

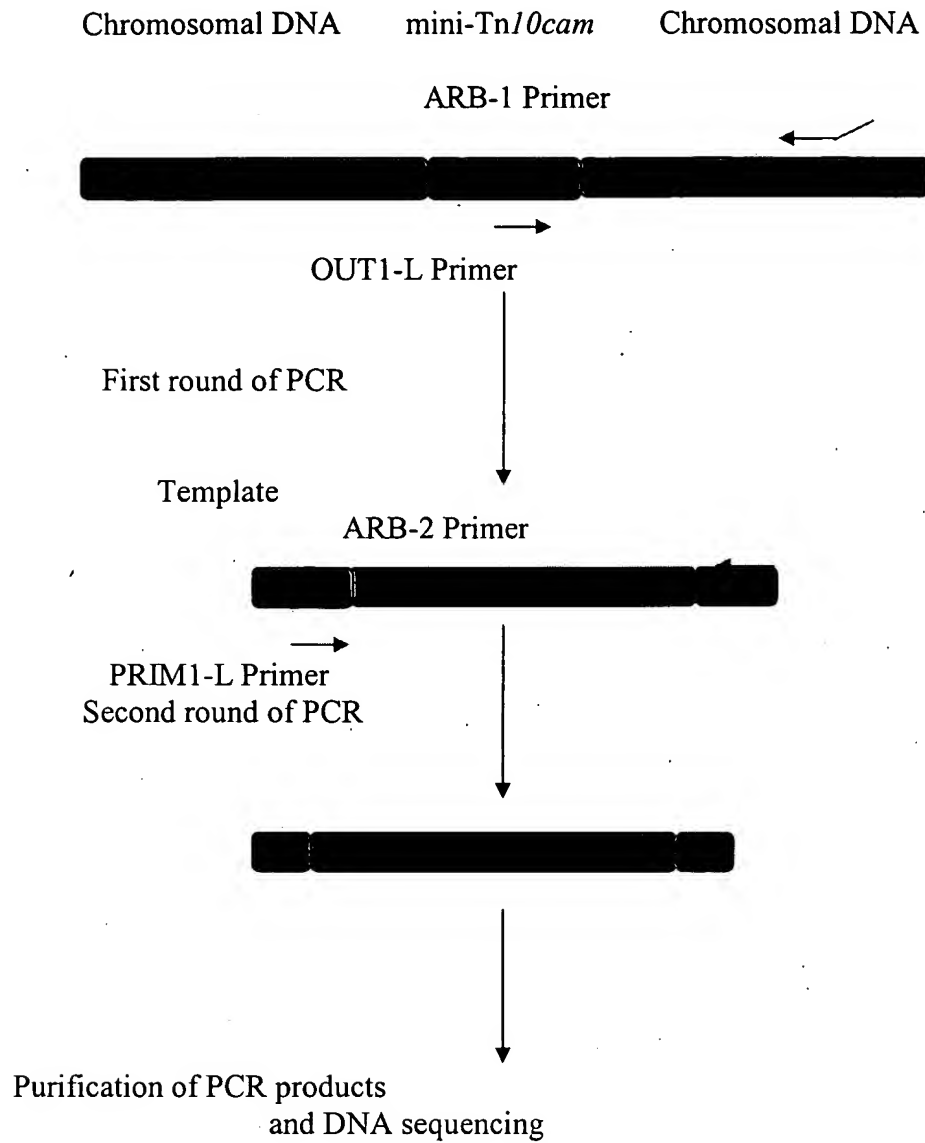
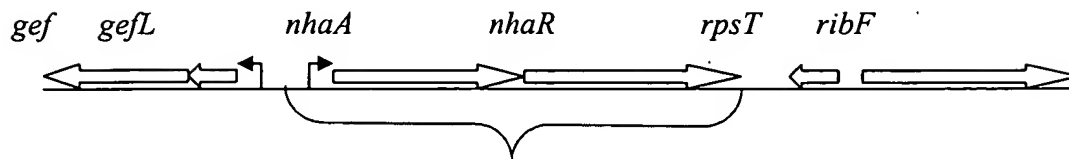
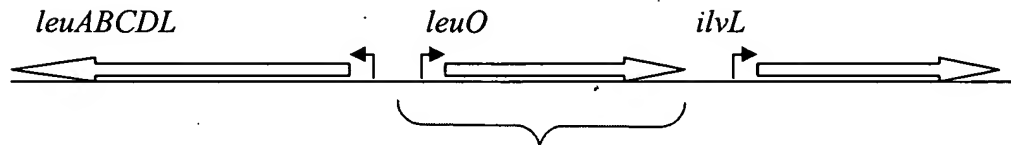


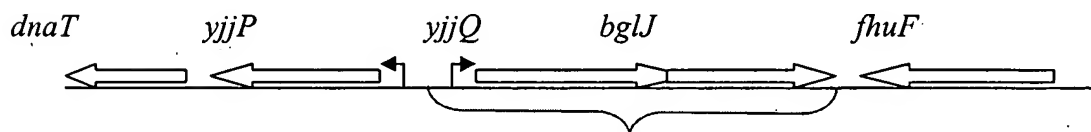
Fig. 1. Schematic diagram of Arbitrarily primed Polymerase Chain Reaction



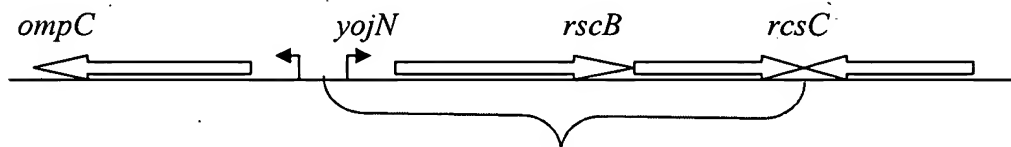
Genome included in cloning *nhaR*



Genome included in cloning *leuO*



Genome included in cloning *yjjQ*



Genome included in cloning *yojN*

Fig. 2. Genes or operons for complementation studies. Open reading frames or coding regions (\rightarrow); predicted promoters (\curvearrowright); cloned regions ($\underbrace{\hspace{1cm}}$)

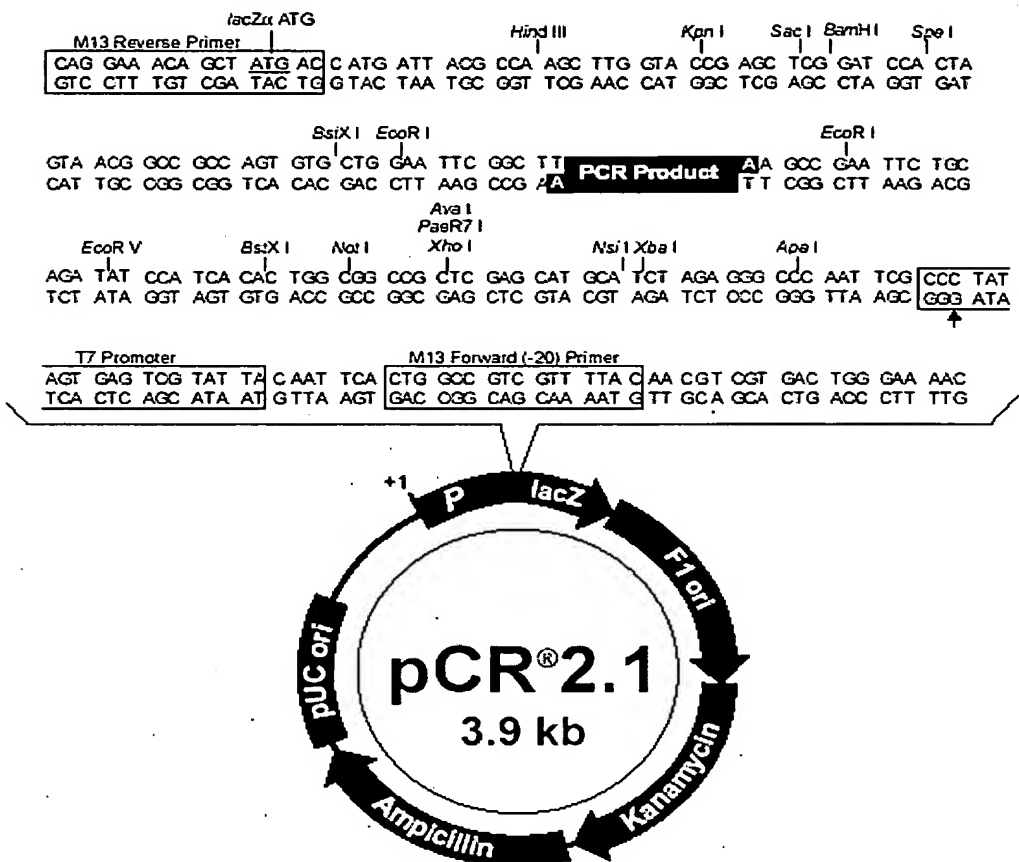


Fig. 3. Vector pCR2.1 with insertion cloning site and resistance gene for Ampicillin (Invitrogen, Carlsbad, CA)

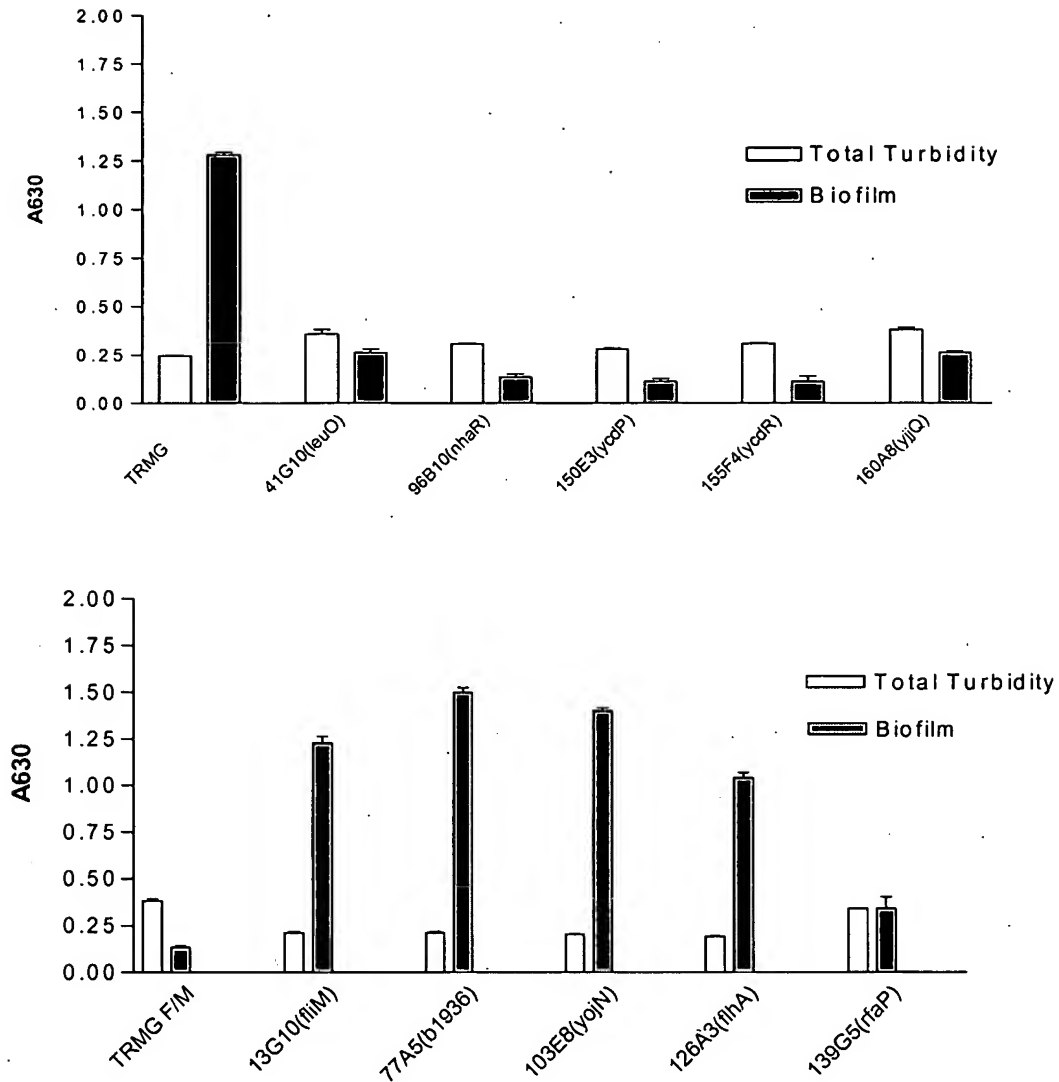


Fig. 4. Cell Growth (total turbidity at A630 before staining) and biofilm formation A630 after crystal violet staining) absorbance readings for parent strains and representative mutant strains.

- A) TRMG parent strain and biofilm-down mutants 41G10, 96B10, 150E3, 155F4 and 160A8 TRMG F/M parent strain and biofilm-up mutants 13G10, 77A5, 103E8, 126A3, and 139G5 (Upper Figure)
- B) TRMG F/M parent strain and biofilm-up mutants 13G10, 77A5, 103E8, 126A3, and 139G5 (Lower Figure)

Fig. 5

Sequences of Up Mutants

1B10 (10X)

fliD gene - flagella biosynthesis; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

AAAAACGGTTACCGGATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTC
ATCAG
GGTCAGGTCTGGATTTAAGTTCCATCCTTGATAGCCTCACCGCCGCGCAAAAAGCGA
CGCTAACCCCCATTTCAAATCAGCAATCGTCGTTTACCGCTAAACTTAGCGCCTACG
GTACGCTGAAAAGCGCGCTGACGACTTTCCAGACCGCCAATACTGCATTGTCTAAAG
CCGATCTTTTTTCCGCCACCAGCACCACCAGCAGCACCACCGCGTTC

12E12-6 (7x)

rfaG gene - enzyme, macromolecule metabolism; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # S75736

Protein Accession # AAD43826

AAAAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTCCCATACCAACCATGGACGCAATGCAGAATATTATGCCTGGGTACAAAATCATCTCAAAG
AGCATCCCGCAGATCGCGTTGTTGGGTTTAATAAGATGCCTGGCCTGGATGTTTATTTTGCCGCTGATG
TTTGTTACGCCGAGAAAGTTGCGCAAGAAAAAGGTTTTTTATATCGTTTAACATCACGATATCCNCNN
NNNNNGTACTAGTCGACGCGGGGCCAANN

13G10-4 (11X)

fliM gene - Structural component; surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NAAAAACCCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGTTCAACCTGCTGCGTCGTAGCCCGGATATATCCNNCNCNCNGNACTAGTCGACGCGTGGCCA

14C10-4 (10X)

flgE gene - structural component; surface structures/ flagellar biosynthesis, hook protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74160

AACGGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGATCANCTGAATTCCAGTGATCCGCTTCTACTGTTACGCCATTCAANNGCCNGCAATGCGGNTANCTNTNAC
AAANAAGGTTNNGTGACTGTTTTCCACAGTCATGGTAATGCTCATGACATGAGCGTCTACTTTGTGNACCCGGG
GATAATAACTGGCAGGTCTACACCCAGGATAGCAGTGATCCAAACAGCATTGCGAAGACAGCG

36E2-5 (3X)

yhjH gene (complement) - orf; unknown function ; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_004431

Protein Accession # NP_417982

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCTTACACCTGGCAGCCGATCTATCAAACATGCGGGCGGTTAATGGCCGTGGAGCTATTAACGGTGG
TCACGCATCCCTTGAACCCCTTCGCAACGCCTGCCGCCGGATCGCTATTTACTGAAATCACCGTCAGCC
ATCGGATGGAGGTTGTGAAAGAGCAGATTGATTTGCTGGCGCAAAAAGCCGACTTCTTTATAGAGCAC
GGCCTGCTGGCATCGGTCAATAT

38G7-2 (11X)

flhM gene - Structural component; surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTTCGGTATGGGTAAACTCGCGACCTTCCA
CTTTGGTTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAG
AACACCACCAGCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTTCAGGTTGGTCGGCACCGGCAG
GTTGCGGGCAAATTCATGGTACGGCTGAATGCGGATGGCCCCGACGGTTATATCCNGNCNNNNNGTAC
TAGTCGACG

39C9-2 (3X)

rep gene - enzyme; DNA replication, repair restriction/modification; product - rep helicase, a single-stranded DNA dependent ATPase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000454

Protein Accession # AAC76783

AAACGGTTACCGGATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCAT
CAG
TATCCAGCCCCAACGTATGGAAAGTGGAGATCATCAGCCACGCGCCTCTTTGCGCCCCAGCGTCTGC
CCTACACGCTCTTTTCATCTCGCGCGCTGCTTTATTAGTAAAGGTCACCGCCGCAATGTGCCGCGCCTGA
TAACCGCAACCGCGGATCAGATGGGCGATTTTATTGGTGATAACACGAGTTTACCGGAACCCGCGCC
CGCCAGCACCAAGCAGGGGCCGTAACGAATTCGACAGCTTGTTGTTGGCCGGGGTTTAGACGCATAG
GTGTATTGCTCA

42G6-4 (12X)

flhP gene - putative structure; surface structures/ flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG

TGGTACGCATCTACATAAATTTTGTCTGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAG
CCCCAGCAATACCTGGTTAGGTGGCGCGCGGAGGGTGTTCACGCAATAAACCAAAAAAC
AATGATGATGCGGGTGAACCTGGTCATCATCAGTAAATTTGCCGGAATAAACGTCAACGAGGTGATG
AACACCAGCGTCTGCACCGGGAGC

43B10-3 (11X)

fliG gene – Structural component; surface structure, flagella motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

NNCNNAACANACGGNNCCGGCCNG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGGCGAGCTGGCGCAGAAAATCATCGACGAGATGTTCTGTTCGAGAATCTGGTGGATNTCGCCAATCGCNGT
ACTAGTCGACGNGTGGCCAAANTGGATTCNAATCGCTGNTGATCGCGCTGAAAGGAGCCGAGCNGTCACTGT
GCNAGAANTTTCTTGCNCNATATGTGCNCNCGTGCCGCCNATATCCCNCCNACCGTACCCCTNGNACGNNNN
ACCNGNACCCCNNTNCGGNCAAGNATGNNANNANCCNGATANANCAAGNNCANTNCTNNGATNCACNNNATAN
NANNGNCGCCNAC

43F5-2 (2.5X)

wecB gene - enzyme; Central intermediary metabolism; sugar-nucleotide synthesis, product - UDP -N-
acetyl glucosamine-2-epimerase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000455

Protein Accession # AAC76791

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTCAGGCATGCTCTCGCATTCTGGAAGCGTTAAAAAATAATCGGATATCACTATGAGTTTTGCGACC
ATTTCTGTTATCGGACTGGGTTATATCGGGCTGCCAACNGCTACNCGACNCGCGCCNCGGCAAAAACA
GGTAATTGGTGTGATATCAACCAACATGCGGTTGATACCATCAATCGTGGCCAAATCCATATCCCCC
CCCCCGTACTAGTCGACG

45C8-4 (4X)

frdA gene – enzyme; energy metabolism, carbon: anaerobic respiration; product is fumarate reductase, anaerobic
flavoprotein subunit

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000487

Protein Accession # AAC77114

CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGCGCACGGCAAATCCGAATGCAAAAATCGCACTAATCTCAAAAGTATACCCGATGCGTAGCCATACCGT
TGCTGCAGAAGGGGGCTCCGCCGCTGTCGCGCAGGATCATGACAGCTTCGAATATCCCCNNNCCCCCGTACTA
GTCGACGCCGTGAANANNNN

49G9-3 (12X)

fliP gene - putative structure; surface structures, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

AACGTACCGGATCCGG

GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCAGAC
TGGCGAATATCGGCCCGTTGCGTNTACTCNACNCGTGCCNATGCGCATTTTGCTNCCNGCCTACGTGA
CCAGCGAGTTGAAAACCGCATTTTCAGATACGGCTTCACAGATTTTCATCCCTTTTTTGATTATCGACCT
GGTGATAGCCAGCGTGTTGATGGC

51B12-3 (6X)

flhM gene - flagella gene, flagella biosynthesis; motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

ATGAAAACGNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TACTCAACTTCCAGCGGATTAATCGCCTTCCAGGCGTCGCTATAGCCTTCAAGCGCCAGTTTCAACATG
CGGTTGATGACGCGCTGTTCCGGTATGGGTAAACTCGCGACCTTCCACTTTGGTCGGGAAGCGTCCATC
GCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAGAA

57E7-6 (7X)

flhP gene - flagella gene, putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCAGA
CTGGCGAATACCGGCCCGTTGCAGGGACCTGAAGCCGTGCCGATGCGCATTTTGCTCCCGGCCTACGT
GACCAGCGAGTTGAAAACCGCATTTTCAGATAGGCTTCACGATTTTCATCCCTTTTTTGATTATCGACCT
GGTGATAGCCAGCGTGTTGATGGCATTGGGGATGATGATGTT

61G2-3 (10X)

255 bp down stream of flhB gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834

NGNNNATACGNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATTAAGCGTGAATGATGCCAGAGCGCAAAGCGTTCAATGGTTTGAGTAAGGGGCAAAACAGGCGGG
ATTTAGGGCTTTTGCTGCCACATATCCNNNNNNNNNGTACTAGTCGACGCGTGGCCA

63A9-1 (4X)

rfaQ gene (complement) – enzyme, macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_002695

Protein Accession # NP_312534

AAACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATGTGTACCGTGATTGGCGCTAAGNGTGNGAAGCTTTTTTTTCCAANTACCATGCTTGCCNNATGACC
ATAANGTTGCGATATNTTCATTCCGTGCATGCAAACANCGTACCNNCAGCGCCACCATNCAACTGATG
CGTCNGANTAATGACCAGGTTNTANTTATTCTNTCGCCGAGCCTCATCANCNAANGCTCNCTTTNTNN

NCGGN\NNNNNATTTTNCNCGTCTNNNTNTTGNNTNANTNNNTTACGCGGCNACNNATTNGTTNTGG
TCNTACGNCGCNNNATAACNCGCNCNCTCNCNNCC

64F2-1 (9X)

factor Sigma32 – promoter dnaKp2; documented +1 site at 12121

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D10765

Protein Accession # BAA01595

CGNCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CGTTTCGCCCCATTACAGACTCACAACCACATGATGACCGAATATATAGTGGAGACGTTTAGATGGG
TAAAATAATTGGTATCGACCTGGGTACTACCAACTCTTGTGTAGCGATTATGGATGGCACCCTCTCG
CGTGCTGGAGAACGCCGAAGGCGATCGCACCAACGCTTCTATCATTGCCTATACCCAGGATGGTGA
CTCTAGTTGGTCAGCCGGCTAAACGTCAGGCAGTGACGAACCCGCAAAACACTCTGTTTGCATTA
CGCCTGATTGGTCGCGCTTCCAGGACGAAGAAGTACAGCGTGATGTTCCATCATGCCGTTCAAAAT
TATTGCTGCTGATATCCNCCCCCNG

66F4-3 (10X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

TACCGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTCCGATATGGGTAAACTCGCGACCTTCCA
CTTTGGTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAG
AACACCACCAGCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTTCAGGTTGGTCGGCACCGGCAG
GTTGCGGGCAAATT

67C8-4 (6X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NNCGTNCGG
GATATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTCGGAA
ATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTCCATGT
GGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTGAGCATGATCGAGCCGCTACGGG
AATTGTTGGTTAACCCGCC

67C9-6 (8X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

ANCCGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG

CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTAC
GTGCGTTTCGGAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATT
GTGGTTAACACGCCGTTCCATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATC

67E10-5 (6.5X)

flil gene – Enzyme, flagella synthesis; surface structures, flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75008

CGNCCGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CACCTGCAATTCGAGGAGCGGAGAAACATCCGCCGAGCGGCAATCACCCTGAGCGTGCACGCCCTTCGGC
ACCGAGGATGTTCTCAATAAAATCTTTTACTTCGCGCCACGTTACCAATCAAACCCACGACAATGATATCCN
NNNNNNNGTACTAGTCGACGCGTGGCCAAT

70G12-5 (5X)

flil gene – flagella synthesis, enzyme: surface structures; flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75008

TANGAAAAACGTACCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGCTCCAGCCCCTGGAGAGACGCTTNCCAGTCCGCGCGTTCAAAAATGCCTTGTTGCAAATAGCCCTCCAGCTG
CGGCCACAGGGCGATGGCTTTATCGAGCATCGGATCGCTGCCTTTGGCATAACGCGCCGACGCTAACAGATCGC
GGTTACGCTGAAAACCTCGACAACAGCTGTTTGAAGGTGCGCACTCGCGCGTAATGTTGCTCACTGATCAACGCC
GTCATTGCGCGGCTGATCGACGCTTCAATATCCNNNNNNCENNNGTACTAGTCGACGCGTGGCCA

71A4-3 (10X)

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP_418089

AGCNCGCCGGACNTCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTCGCTAGTGGAAGGCCATTTGAAAAATCCTGGTCATAAAGATGCGATATCCCCCACCAGCGTAC
TAGTCGACGCGTGGCCANANANNNNNNNCGGCANNCCNCCCNT

74B5-2 (2.5X)

rfaG gene (complement)- enzyme, macromolecule metabolism, LPS; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # S75736

Protein Accession # AAD43826

ATACCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGCATTCATCAACAGTTGCCGCACGGGGCCACCATGTTTCGGGTATATACACAGTCGTGGGAAGGCGA
TTGCCCCGAAAGCATTTGAGCTTATTCANGNGCCAGTTAAGTCCCNACCAACCATGGACGCAATGCAG
AATATTATGCCTGGGTACAAAATCATNTNAAACAGCNTCCNCAGGATCTGTGTGCGNNGNGTTCAATT
ATTATNCCCTCGNCNGGATTATCTTATTTGCCTGCTNAATGTCNGTCTTCTNATTCCTAAATNT

76F11-2 (5.5X)

fliM gene - flagella gene, flagella motor switch biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NGAAAACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTCGGAA
ATGCAGGTGAAATTTACCAATATCACCACTCGCCGAACGACATTGTGGTTAACACGCCGTTCCATGT
GGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTCAGCA

77A5-2 (11X)

b1936 gene - orf; unknown function; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC 000913 (genome)

Protein Accession # E64957

CNCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ATTCAGGTGCGTAATAAGCTGGTGGCGCGTATCAGGAAGTGATGAGCATGCAGGTGTAGGTTTTGTA
ACCTGTTGTTAATTACATCCGATCTCACCGCGTGGGGCATGGATGGGGCAAACCTCACTCAATTTCTGGT
TTAAATGGATACCTGATCCTGAACGTTTTCTGCCATCCACGATCCGTATACGCGATAACCCCCCTGAA
CATCAGAGCGTCTCA

78E3-2 (7X)

fliA (complement) - flagella biosynthesis, alternative sigma factor

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74989

NAAAACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGGTTAATACCAGTTTTTCGCGCTCCGGCAACGTTTCGATGGCTTCCATCACCCGCTGGCGCAGATTAC
TGTCCAGTAGTTGTTGTAGCGGGTTTTCTCGCTGATGATCATCAGTAACCAAGTTCGATGCTATCGCCGT
GCTCTTCGCGCCACTCATCGTAGGAGAAGAGCTGGCTGTTATTGGTGTGAGCAACATTTGGCGATAA
TCGGCAATATCNCNCCCCCCCCGTAAGTACGACGCGTGGCCAA

78F6-3 (2X)

tolA gene - membrane; colicin-related functions; membrane spanning protein required for outer membrane integrity

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000177

Protein Accession # AAC73833

ATACNCGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTAGCTGCTGCCAACGCAGCCTGACAAAGTGCGGGATCGCCACCTTCAGGTTTGATATCCAGTAA
CATAACATCGGGTGCCAGTTTTATGCGCAGCGTACAGGTTTTGCCTGCATAGGACGATGCGTCATAGA
ACTTACTTTTCGATAGCAGATTTAATCTGCCCGGCATAGTTATTGATATCCNCCCCCNNGTACTAGTCG
ACGCGTGGCCANNTATTNCGATATCNCNCCNGCCNGTCTANTCCNCGTGGNCATATCTGATNC

85G11-1 (6.5X)

Between 2 promoters (complement) - 1) factor sigma 70; predicted +1 site at 201135 and 2) factor sigma 70; predicted +1 site 2011238

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D89826

Protein Accession # AAC75005

ANNGNAANAGCNCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTCTTGNTCCACTTTGCCAATANCGCCGCCNTAGCNCTAGNCGNCGCACGNNCAGACGCGTGGCCA

89A8-3 (6.5X)

fliG gene - flagella structural; flagellar motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

CGNTACCGGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCTCGGCTCCTTTT CAGCGCGATCAACAGCGATTTCGGAATCCACTTCCTGCAACAGACGCTGAATGCT
GCGATCGTCGACATCCACCAGATTCTCGAACAGGAACATCTCGTCGATGATTTTCTGCGCCAGCTCGCC
GTCGAATTCACGCACGGCGGTAATAACGGCTTCTTCCTGCTGAGTTTTC

92G7-3 (3.5X)

mhB gene - enzyme; degradation of RNA; product is RNase HII, degrades RNA of DNA-RNA hybrids

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

GGAAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCAGCGCCGCCNTTNNNG
CGTCACGCGTNACTTTCGCCAGGATAGACGCGGCACTGATTTCCGGTACGCGGCTATCGCCTTTCACCA
CAGCCATCGCAGGCATCGGTAATTTGCGGCAGCGGTTACCATCAATCAACACATATTCCGGCGCAATA
TGCAGCCCAGCGACGGCACGCTGCATCGCCAGCATGGTTCGCATGAAGAATGTTTCAGCTCGTCGATATC
CNNNNNNCNCGTACTAGTCGACGCGTG

92G9-1 (3.5X)

mhB gene - same clone as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

TANGAAAAAACGTTCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCNCCNCCNNGTACTAG
TCGACGCGTGGCCAAATATNNNNATATNNNNNNNNNNNNNNCTANNNNNCNCNGGNNANNNN

94G6-3 (4X)

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP_418089

NNNGNAAAGCCCGCCGACNTCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTCGCTAGTGGAAGGCCATTTTCGAAAAATCCTGGTCATAAAGATGCGATATCCNGNNNCCNNGTAC
TAGTCGACGCGTGGCCAAAANNNCNNNNNNNANNNCNATNCTNGCNCCCNNCCANC

98E7-4 (6X)

fliR gene - putative enzyme, surface structures; flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75017

CGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACTGAATCTGGCATTAGGTTTACTTAATCGTATGGCCCCGCAATTATCCATTTTTGTTATTGGATTTCCATTAA
CTCTGACTGTCCGCATCTCTTAATGGCGGCATTAATGCCGTTAATTGCACCTTTTTGCGAACATTTATTCAGTG
AAATTTTAAATTTGCTGGCTGATATTATTAGTGAATTGCCATTAATATAATTCCGTAACGTTTATCATGTTATCCT
AAGGATTATCCGAAAAATAACCTACGAACATCTTCCAGGATACTCCTGCAGCGAAATATTTGTTTTAAGCTC
ACTCACATATCCCNNCCNCCNGTACTAGTCGACGCGTGGCCA

98E11-3 (5X)

flgH gene - structural component, surface structure; flagellar biosynthesis, basal body outer-membrane L (LPS layer) ring protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74163

AACNAAACGGNTNCGGCATCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAGC
GCTGCGCATACTTATGCCATATCCNNCNGNNGGTACTAGTCGACGCGTGGCCANATTNNNNNATCNN
CNNNNNNGGGGCGNN

98G12-4 (5X)

mdoG gene - enzyme, osmotic adaptation; periplasmic glucans biosynthesis protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000206

Protein Accession # AAC74132

AAACGACCGGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGGGCAAGTTGCTTTTGGGCGTCTCGTAGCCTTTCCCGGCTAAAGATTGAGCTTGCTTTGCGACATCAT
CAATACTGAAAGCCCAGCTTGAAGATGTATACAGGGTTAACATTACTGCAGCACTCAACCAACGCATT
TTCATTATTTGTAGCTTATGTTTCATAATTAGTAAGGCACTTCCCCCTTNGTGTGCTTATATCCCTNNG
NTNCCNTNCTAGTCNACNCGTGGCCACTNCTATCCNGNNNTCCCCGNTNNGCAGTANTCAGAC

103C8-4 (9X)

fliP - flagella biosynthesis, surface structure

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

GANNAAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGCGCCCCCTTTTTCCAGCGCCTCCTGCATTGATATTTTCTCTTCGCTGAATGGCTGGTACGCATCTA
CATAAATTTTGTGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGCAATACC
TGGTTAGGTGGCGCGGAGGGTGTTCACGCGCGTTACGCAATAAACCAAAAACAATGATGATGCGGG
TGAAACTGGTCATCATCAGTAAATTTGCCGGAATAAACGTCAACGAGGTGATGAACACCAGCGTCTGC
ACCGGGAGCGACCAGCTTTGTCCACCGCCAGGCAGCG

103E8-4 (7X)

yojN - putative regulator, not classified; product is putative 2 component sensor protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000310

Protein Accession # AAC75276

NATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTGCAACCTGTATCACACCCGATGAAAGATTAAATTAGTCAAGATTATGATATCTTTTTAACGGATAAT
CCGTCTAATCTTACTGCCTCTGGCTTGCTTTTAAGCGATGATGAGTCTGGCGTACGGGAAATTGGGCCT
GGTCAATTGTGCGTCAACTTCAATATGAGCAACGCTATGCAGGAAGCGGTCTTACAATTAATTGAAGT
GCAACTGGCGCAGGAAGAGGTGACAGAATCGCCTCTGGGCGGAGATGAAAATGCGCAACTCCATGCC
AGCGGCTATTATGCGCTCTTTGTAGACACAGTACCGGATGATGTTAAGAGGCTGTATACTGAAGCAGC
AACCAGTGACTTTGCTGCGTTA

104G4-5 (2.5X)

Between mreB and yhdA genes (complement). mreB: phenotype, cell division; regulator of ftsI, penicillin binding protein 3, septation function. yhdA: orf, function unknown, hypothetical protein, 1232 bp upstream of mreB

Transposon Tn10 Accession # AY528506

Nucleotide accession # M22055

Protein Accession # AAA83892

ANNNNCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCANAATCATTAGGGGATTNATCAG
CTNAATGCATGCNCNACCATTGCCTCNGCTGTTTGCAACCGNGTAAGGNGCATTTCATNTGCATATGTT
GCTGCNANCAATCTGGCTGAGNAGACAAGCNCACCTCCCATGANACGCATCGCGCATTATTNTACGTGA
AANCGGATNNAANGGNTGGNTAAACCNANGANCNNCGCCGANTATNNTTCCNCTGNCANNCTNANN
TNGNCTNGNACNGANNNCNANNNCACNCCTCTTTNTNNNNNTCCGNTNNNGNNGNNNNNNNTNGTNN
TCCNNCCTGTNTNCANNTNNCNNNGNTCNTNCNCCNTCTNTCCANTGCCANTTGTNNCNAGGTNCGA
TNTCTGCNGACCNACNNNNTAGNANCCNN

107B12-2 (2.5X)

Upstream of promoter - factor sigma 70; predicted +1 site at 3806141

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # AAC17834

GNAAANCCCGCCGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGGATTTTACCAAAATCATTAGGGGATTCATCAG
GCGGTAGCGTGCTTTTTTCTGCTTAACCTTAACCAGACAATCACACAAAAGAGTCGCTAGTGGAAGC
CATTCGAAAAATCCTGGTCATAAAGATGCGATATCCNNNNNN

110E8-3 (6X)

fliP gene - Putative surface structure, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

AACGCTNCCGATCCG
GATNATATNAACAGATNTGTATNCACCTTATCTTAATGANATTTTACCANAATCATATTGGGGATATCATAT
ANGGGCTGCCCCCTTTTTCCAGCCCCTACTGCATTGATATTTTNTCTTCGNTGNATGG
CTGGTACGCATCTACATAANTNTTGACGATCACCGGTGACNTAATAAAANAGGNCN
NANNCANTGCCANTCCCAGCAATNCNTGGTTNNGTGGNGCGGACGGTGCTNCCATN
GCNNGACNCACNNAACCNANNNCNATGANGTNCNCNCGANANTGGANATCATCC
TGCAANNCNACNGNATNCNNA

110F12-2 (9X)

Between flhD and insB_5 genes (complement)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834, AAC74963

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGATNANCTGCAATAAGCAGAACCCCTTTTTGGNTTAATATGTCCTTACAATAAGAAATGGGTCTTTACACTT
ATCTAAGATTTTTCTATATCNCNCNCCNNGTACTAGTCGACGCGTGCCATTTATNNNNNATNTCCTNNTNG
TCTCNNGNNCNNCNCGCGCCNCANCNNNATATNNNTNNNNCNCNTNCACTCTN

111G8-1 (4X)

flgK gene - structural component, flagella biosynthesis; hook-filament junction protein 1

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000209

Protein Accession # AAC74166

AACCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGGGTGGCAATGGTGTCTACGTTTCTGGTGTGCAGCGTGAGTATGATGCGTTTATTACCAACCAG
TTACGTGCGGCGCAGACGCAAAGTAGCGGTCTGACTGCCCGCTATGAGCAGATGTCGAAAATCGACA
ATATGCTCTCCACCAGTACCTCTTCGCTGGCAACACAGATGCAGGATTTCTTCACCAGCCTGCAAACGC
TGGTGAGTAACGCGGAAGACCCGGCAGCGCGCCAGGCGCTGATTGGGAAATCAGAAGGATTGGTGAA
TCAGTTTAAAACACCGATCAATATCNCNCCNCCGCTACTAGTCGACGCGTGCCANANNATNCT

115A3-5 (2.5X)

flhD gene – flagella biosynthesis, surface structure; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

ATACCGATCCGG
NTCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GCTTACGCCTGCTTTTTCGCTTGTGATGGCATCACGGATCCCGCTTAACGATGAGTTAGCCGCGCTGAT
ATCAATGGTNATCGTACTANTCGACGCGTGGCCATGAATGGTGAGTTTACTGTCGCTGGTGGCGATCG
CCGTTTTTCATATCGNCNNTTNCNGTACTAGTCGACGCGTGGCCAAATTNNTNTNANAAAAATTCTN

115B7-6 (7X)

flgB gene – flagella biosynthesis, cell-proximal portion of basal-body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

AACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCGCGATATCGATTTTGCCAGTGAACCTAAAAAAGTCATGCAACGTGGACGGGATGCAACCAGTGTG
GTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGCCTCCTACCGCAGAACT
GCAATACCGTATTCCGGACCAGCCTTCGCTTGACGGTAATACCGTCGATATGGATCGCGAACGCACCC
AGTTTGCCGATAACAGCCTGCAATACCAGATGAGCCTTAGCG

122F6-1 (4X)

fliL gene - flagella gene; putative surface structure

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75011

CGNTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACGACGCGTTGCTGCGCTTTGTCGTCAGCGGCAACCTGATGCGAATGCCAGTAGCTGTAACCTGCGC
TGGCACAGGCCGCGAGGGTAATGAATACCAGAATCGGGATCCAAAGCGATCGCTTTCTTGCTT
ATCGCGTAATCAGTCATGTGTTGCGGTCTTCCTGTGTCGCTACTGCTTATC

123B8-4 (3.5X)

rfaQ gene (complement) – Macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_002695

Protein Accession # NP_312534

AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTAAGTGTGTGAAGCTTTTTTCCAAATACCATGCTGCCGATGACCATAAAGTTGCGATATTTTCAT
CCGTGACAGGTAAACAACGTACCAGCAGCGCCACCATCCACTGATCCGTAAGATTAATGACCAGGTCAT
AATTATTCGCACGCAGAGNTTTATCAACNAAAGCACATTTTTAATTNATCGAAAGTTCCNCNCCTT
TATTGCTTANCCCATAGAGCGCANTNNTTTCGGGTTTNCANACAAAATNTGGATGGTGNCCTGNCNA
AGCNNCANGTCTANNTNNGCTNTATGAGAATCTG

123E4-3 (6.5X)

fliR gene – putative enzyme; flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75017

AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTTACCCGTTTCGGTACGCTGCGTTCGCTCAGAAATCGGCGCGGTGGAGATCATCGCCAGCTCNCGC
ANTNACGGNCAGAAANTACAGGTTTAACCAAGGATAGCCATTGTTNGCTTGCCACCTGCANCATAGTACG
GTTACCCNATGATTTACTNGNAGGTTAGTGAACAANGTGC GGNCAGTNATTCAACAACACATTNNGCA
TGNTCTGTCTNGGCANNTATTTTGGTGATNAANANGGCCGATNNTTTTNCGANTNNCCGNNNTGGGNT
NCTTNTTCATCNAGTNNCANNATGGGCGNGTATN

125C9-2 (7X)

fliP gene – Putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

TACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGCGCCCCCTTTTTCCAGCGCCTCCTGCATTGATTTTTCTCTTCGCTGAATGGCTGGTACGCATCTACATAA
ATTTTGTCTGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGCAATACCTGGTTAGGTG
GCGCGGAGGGTGTTCAGCGCGTTACGCAATAAACCAAAAACAATGATGATGCGGGTGAAACTGGTCATCAT
CAGTAAAATTGCCGAATAAACGTCAACGAGGTGATGAACACCAGCGTCTGCACCGGGAGCGACCAGCTTTGT
CCACCGCCAGGCAGCGCTGGCTGGTGATACCCGGCAGTTGCGCGAAGGCGAGGGGCGTAATCAGCCAGAGA
AGGACAGGTGCGACAGACAATAAACGACGCAT

125F2-4(3.5X)

rfaQ gene (complement) – enzyme; macromolecule metabolism: LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_002695

Protein Accession # NP_312534

GNGNAAAAACGTNCCGG
ATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGGTGTCTGATAAAGCAGCATATCGATTTTTGCATCANGATAATTCTGCTTGAGCGTACTGATGAC
AGGAGTAGTTAATAACATATCCCCATGATATCNCNNNNCNGTACTAGTCGACGCGTGGCCA

126G2-2 (7X)

fliA (complement) - flagella biosynthesis; possible export of flagella proteins

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74949

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCGAACCTGGTATTTTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTGGTG
GATACGCGGACGCGAACAAGCGCCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAATAATACC
GTTGTCTGAAGCGACGTGGAACGATGTACAACCTGGAAGATTCTCTGGGAATGGAAGTGGGTTAT

GGACTGATCCCGATGGTTCGATTTCACGACGAGTGGTGAGTTGTTGGGCCGTATACGCAGTATCCGCAA
G

126A3-2 (7X)

flhA gene (complement) - flagella biosynthesis, possible export of flagella proteins

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74949

ACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCCGAACCTGGTATTTTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTGGT
GGATACGCGGACGCGAACAAAAAGCGCCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAATAATAC
CGTTGTGCAAGCGACGTGGAACGATGTACAACCTGGAAGATTCTCTGGGAATGGAAGTGGGTTATCGAC
TGATCCCGATGGTTCGATTTCACGACGAGTGGTGAGTTGTTGGGCCGTATACGCAGTATCCGCAAGAAA
TTTGCCAGGAGATGGGATATCN

132B8-2 (7X)

fliM gene - surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NTNNNAAAACACGCCGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTTGCCCGCCATTTTCGTATGGGGCTGTTCAACCTGCTGCGTCGTAGCCCGGATATATCCNCCNGG
NGCGTACTAGTCGACGCGTGGCCAANNNNNNNNCNCNNCTAGCNNTAAAANNNGNCATNANCCNCNC
NCACAANACANNANGNANNCNTTNCNAAACNANCGTANNATANCCCCNNC

136E3-1 (7.5X)

arcB gene (complement) - enzyme, Global regulatory functions, aerobic respiration sensor- response protein; protein kinase/phosphatase, sensor for arcA

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000400

Protein Accession # AAC76242

NNAAAGCCCGCCGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCAAAGCCTGCTTTGANATCCGTAAAGNGCGGACTAANCNACNCGNGGNCNAA

139G5-3 (5X)

rfaP gene - enzyme; macromolecule metabolism: LPS; phosphorylation of core heptose, attaches phosphate containing substrate to LPS core

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000440

Protein Accession # AAC76654

GNGAAAAAACGNACCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTTAAATCCATTAACTCGCGCATCATTTATTATTACCGAAGATCTCACTCCCACAATTAGCCTTGAAGATTATT
GTGCCGATTGGGCAGTCAACCCGCGCTGATATCCNGNNCNNNNGTACTAGTCGACGCGTGGCCATANANTNAGC
TCNTNCTACNNCCNANTCCTATCCACCCGTGGCTNCAGNNANCATTTCNGNNNACACCANTTACNNNCCAGNC

CNCNTCCCCNGNNCTCANNCTACTCANNACTTCANNANANNATGNCNTTCNNNNNGCENNNTCGNTCNCCCACNA
CNNCNTTTNTTNCNNCCTCTNNCNANCTCNNCCNTNNCNCNTNTNATTCNCCTTTTACCCTNAN

152B4-6 (9X)

flgI - flagella biosynthesis, putative surface structure; product is homologue to P-ring of flagella basal body in Salmonella

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74164

GNNGAACGNCGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CACTTTGCATTGATTGCAGTATGGACATCAGATCCATCGGCGTAGCGCCCAGCGCATTGAGCGCGCGC
ACCACGTTATTGAGGCTGGCGCTGGAACGTACGCTTTGCAGCGAACC GCCGCTCTGGCGTAAATCGAT
CTGCGTTTGTGGAGTAACCACAGTCTGTCCACCACCAACGGTGTATCTGGCTGGCTGACATTGGCCTG
ACGATTAAGTGTACTGAGAGATTCCCCTGCGCTACCGCGCAGCTGTGAGGGTCACTTCGCGATTTCAT
CACCACCGAACCGGTGCGCGAGTTAATCACTACTTTAGC

163E7-5 (4X)

fliD gene - flagella surface structure; capping protein (same clone as 1B10)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

TNGNAAAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTCAGGTCTGGATTTAAGTTCCATCCTTGATAGCCTCACC GCCGCGCAAAAAGCGACGCTNACCCCC
ATTTCAAATCAGCAATCGTCGTTTACCGCTAACTTAGCGCCTACGGTACGCTGAAAAGCGCGCTGAC
GACTTTCCAGACCGCCAATACTGCATTGTCTAAAGCCGATCTTTTTTCCGCCACCAGCACCACCAGCAG
CACCACCGCGTTCACTGCCACCACTGCGGGTAACGCCATCGCCGGGAAATACACCATCAGCGTCACCC
ATCTGGCGCAGGCGCAAACCCTGACCACGCGCACCACCAGAGACGATACGAAAACGGCGATCGCCAC
CAGCGACAGTAAACTCA

163F3-5 (8X)

fliD gene - flagella surface structure; Capping protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

NNANNAACAATACGTCC
CAAGNANANNTGACNAGANGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCNG
GGNCCGGTCTGGATTTAAGTTTCCATCCTTGATAGCCTCACC GCCGCGCAAAAAGCGACGCTAACCNC
CATTTANATCAGCAATCGTCGTTTACCGCTAACTTAGCGCCTACGGTACGCTGAAAAGCGCGCTGA
CGACTTTCCAGACCNCCAATACTGCATTGTCTAAAGCCGATCTTTTTTCCGCCACCANCAACCACTGCA
GCACCACNGCGTTCACTGCCNCCNCTGCGGGNNAACCCATCGCCNGGAAATACCCCATACCGNTCAN
CCATCTGGCANATGCNGCNAACCCCTGAACACGC

167C2-3 (8.5X)

flgB gene - Structural component, flagella biosynthesis ; cell - proximal portion of basal body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

AAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTCAATCTGCGCGCCAGCGTCAGGAAGTGCTGGCAGCAAACATCGCCAATGCCGATACCCCTGGT
TATCAGGCGCGGATATCGATTTTGCCAGTGAACCTAAAAAAGTCATGCAACGTGGACGGGATGCAAC
CAGTGTGGTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGCCTCCTACCG
CAGAACTGCAATACCGTATTCCGGACCAGCCTTCGCTTGA

Sequences of Down Mutants

1G3-6 (16X)

ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_415541

ATAAAACGGNTACCGGATCCGG
GATCATATGACAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATGAG
GGCGCTGTTTCCACAGCCCTTTTAACGTTTCAGGCATTAATATCCAGCACAGTGNCCTNGNNNNCNCNNNNNC
NTCCACTGATTCAACTGCAGCTTCCAGCTAATATCAATATCTTCGGTGATCATATNAGTCCACNCGGNNCTAGT
CGACGCGTGGCCANNANTNNNNCNTNTTTNTNNCTN

11E4-3 (12X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA (Not Available)

Protein Accession # NA

TTTAAAAACCGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCAGGCGTCTTTTCCGGCCATTGTCGCAGCACTGTAAACGCGTAAAATAGTGCTTTCTCTTACTCTTCTGGCTG
GACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCNNNNCNNNNGTACTAGTCGACGCGTGGCCANANN
ANTNNTATNTTTNANNACNN

12F12-6 (23X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

TTGAAAACCGCTCCGGATCCNG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGTTAAATTGGCATCGTCATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTAATTCTGTGGGATATC
CNNCCNNNCGTACTAGTCGACGCGTGGCCATNTNACNTNCNGCAATNCNTTCTGACACTTCNNNTTNCNTN
AT

14B7-4 (4X)

leuO gene -putative regulator; probable transcriptional activator for leuABCD operon; amino acid biosynthesis:
Leucine

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

GCNNGCGGTAAACGNCCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG
AGTTAAGTGTGACAGTGGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGT
TAAGCAAACCAACANCTTNCGNATGGNCGATTTCAACTTATTAACNCGTTTCGATGCCNTGNTGNAGGA
GCCNANCATTNTTCNCAGCCCGCTCATCGCCCTGGGAACCTTCNCCCCCCTNCNTTCTNTGCTNGCC
TTGGGGCCCCCNCACNCAACGNAGACNGGGCCNATCCC

16C8-2 (24X)

Promoter (factor sigma 70, predicted 1+ start site 1986220); upstream of b1904 (orf, unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AACCGTACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG
TGCNACGNCNCTNTNANNNNCCATNGATNTNGCACTGTAACGCGCTAAATAACGCTTGTNTCTTACTCT
TCTGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCNCNCCGTACTAGTCGAC
GCGTGNCNATATTATGNNNNCCNNNNNCTANTNNNC

24E12-4 (8.5X)

fucA gene (complement) - enzyme, degradation of molecules: carbon compounds: product is L-fuculose-1-phosphate aldolase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC75842

CNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAGAG
GCAAGTGTCAATAATCTGACGAGCAAGTTTATTTTCGTTCCATTAGCTACCTCTCTCTGATTCAAAACAG
GGCAATAATGTTGTTCCCTTTCACACTATTGAATTAGCCGTTTAATTACCCACCATCTTCTTCCTGATTAA
CAAGAAAGAAATTCACAAGCTTATAT

26G11-3 (8X)

ycdS gene - (complement), putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC74109

AACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG
CCAGATGCGTTTCCTGACCCCTCAAGTGAGACTTCATGACGCTGGTTACTGTTCGGAATAATCAGTGAAAG
CCCAGGAGACACCGTACTTACGCCGCTCATTTTGTATACCAGCGAACATAAGCCTGAGCACTGTTGCCT
GTAACACCATTTTTTTCATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCCAGTTGCGAACCAATACG
CCAGTTATCATTAATAATCATACCAGCCAGACAGGCGCGCGCCGGGTTTATGCTCATGATTGAAAACGC
GTTACAGCGTACTCTGCCTCGAGCCAGATATTACG

27F9-2 (2X)

Between promoter (factor sigma 70 predicted 1+ start site 4272977) and yjcC gene (orf, unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTTCATCAG

TGCCCAGGGTTTTTCACCTTGCAATGGCCGGGTATAAACAGGCAGGAAATTGANANCANTGAGNCATN
NNCNACGANACCAATTNCTGGCNTNGCCGGGCATTATCTTTTAAATTCTCTTTCCCATCATTCTTTTCGCT
ATGGATTGCCTTCTTTGGGCAAAATCAGAAGTGAATAATCAGCTCCGAACCTTTGCTCAACTGGCACT
GGATAAATCCGAGCTGGTCATT

31A4-4 (7X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCTTC
ATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTCATTATTGACTGTGCTTTTTT
CGGCTGATGATCTTTGAGATAAGCCGATGCAACCCAATATTGCCCCAGGGCGGAATAATTTGCCCCG
TCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAACGCGCCAAGAT
GATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCTGGGTTATCGTGCCACAGAATTTCTAATG

31G6-3 (2.5X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AAACGACCGGACCG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCNNGCGTNTTTNCCGGCCATTGNCNCAGCACTGNNACGCGTAAATAGNGCTTTCTTACTCTTC
TGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCCCCCCCCG

32A4-2 (14X)

Between ptrB & yebE (complement) - ptrB gene - protease II; yebE gene -unknown function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

NGANNATACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTTGAAACATCTTATAAGGGGTGGCAAACTCACCGGGGATGCAAGCGAAACAGGGGAGTCATTGCT
TAGATGATGACAGGTAATGGCGCGGATATCGAATGTTATGCAANCAGANAANANCAGNCTGTTCAAA
TGGCTGTGCGATTCTGGATAGCCCGAAATAGTCAACTTCAGGCTATCCAGAGAGCGGAATTATTCCGC
CAAAGTGCGTTTTTGTCTGTTTCGAGATCGCGTTCAATGCCGTCACGAACATCCTGGGGGATTTTCAGCGC
GTCACCCAGTGCAATTCAGGTAATGCGTTCCATAAAATGGTCAATATCAATAGCCGCGNNACTAATNN
ACNCGNGGCCNAGCGCCTCTTC

35C6-2 (6.5X)

hscA gene (complement)- factor, chaperone; product is heat shock protein chaperone, member Hsp70 protein family

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000339

Protein Accession # AAC75579

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGACGGTCTTTTGGAGCGTGACGGCGATGGAGAAATCCACCGGCGTTGAGGCGTCTATTTCAGGTCA
AACCCTCTTACGGTCTGACCGATAGCGAAATCGCTTCGATGATCAAAGACTCAATGAGCTATGCCGAG
CAGGACGTAAAAGCCCCGAATGCTGGCAGAACAAAAAGTAGAAGCGGCGCGTGTGCTGGAAAGTCTGC
ACGGCGCGCTGGCTGCTGATGCCGCGCTGTTAAGCGCCGAGAACGTCAGGTCATTGACGATGCTGCC
GCTCACCTGAGTGAAGTGGCGCANGGCGATGATGTTGACGCCATCGAACAAGCGATTAAAAACGTAG
ACAAACAAACCCAGGATATCNCCNNNNCNGTACTAGTCGACGCGTGG

37B5-2 (11X)

yedK gene - hypothetical protein, function unknown

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74998

NGAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CTCCGCGCCCTGGTTTTTAACATTACCCACCGCGCGCGATATCNNNNNNNNNGTACTAGTCGACGCG
TGGGCCAANTANNNNNNCNNNNNTNNNNNNNTNNNNNNCGNNTNNNGNNNNNCNC

41G10-2 (10X)

leuO gene - putative reg of AA biosynthesis (leucine) - Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGTT
AAGCAAACACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAGGAGC
AAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCNCNGTACTAGTCGACGCNGN

41B10-5 (9X)

leuO gene - same as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGTT
AAGCAAACACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAGGAGC
AAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCNC

44C2-1 (10X)

yedS gene (complement) - same clone as 31A4-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG

GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCTTC
ATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTCATTATTGACTGTGCTTTTTT
CGGCTGATGATCTTTGAGATAAGCCGATGCAACCCAATATTGCCCCAGGGCGGAATAATTTGCCCCG
TCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAACGCGCCAAGAT
GATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCT

46E5-5 (10X)

ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GAGCTGGNGCGTTTTCTCCCCACGGCCAGTGGCGTTCACNATAGACCCAGAAATAGACGCCGNCNACAATNCA
CATAATGGACATAAAAAACGGCCAGAAGAAAACGAACCTNATCATCAGTTCACCGAGTGAAAGTACGCTACGC
ATAGGGGTATGCATAACACCAGACATAATATAAAAAACGATACGATGCGATTAA

48A4-5 (20X)

trs5_11 (complement) - IS, phage, Tn; transposon related functions, IS5 transposase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000427

Protein Accession # AAC76530

GAGATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCTCCACCCTGGCCCGATGTCTGGCTTTCATGTATTTCGATGTTGATGGCCGTTTTGTTCTTGCGTGGAT
GCTGTTTCAAGTTCTTACCTTGCCGGGGCGCTCGGCGATCAGCCAGTCCACATCCACCTCGGCCAGCT
CCTCGCGCTGTGGCGCCCCCTTGGTAGCCGGCATCGGCTGAGACAAATTGCTCCTCTCCATGCAGCAGA
TTACCCAGCTGATTGAGGTCATGCTCGTTGGCCGCGGTGGTGACCAGGCTGTGGGTCAGGCCACTCTT
GGCATCGACACCAATGTGGGCCTTCATGCCAAAGTG

49C2-1 (9X)

ycdS gene - (complement), putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GATGAATTACGGGCGATGACAGAGTCATTACCTGAAAATGCATCTACGCAACAATATCCCACNNANTN
GTACTAGNCGACGCGTGGCCATCAACTTGCTGCCGCGATTGACGATGCCAATTTAACGCCAGATATTC
GCGCTGATATTNCTANNCGACGNGCNGGNGACGCGTGGCCAANGCNNNNCNTNNNCTNNNAANNNT
GNNCNGNNCNTGGCTGNTGTCCNNNCTGNNANCGCCNCANAACNTCNTGNCNTNNNNNANGCTGNC
GTCCCTTANNGAAGNGGCCNNGGNNAAATNATGTNNACNCCNTNNCCAANGNTTNNNNACTNNACNA
NCNACCCNNGATNTC

49G12-3 (20X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CACGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
CGTTAAATTGGCATCGTCAATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTATTCTGTGGG
ATATCCNNCCCNCCGCTACTAGTCGACGCGTGGCCATGNNATNNNCCGNNATTCATNCTGATGACNCC
CCGNCAGTTTATANATATNNNNNNNNNNGTNCT

51A10-4 (2X)

modC gene – ATP-binding component of molybdate transport; Transport of small molecules: Anions

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73852

AACGCACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
ACTGACGCGCCCGCAAAAAGGGCGGATTGTCCTCAATGGGCGGGTACTAAATGATGCCGAAAAAGGTATCTGC
CTTNCCGCTACTAGTCGACGCGTGGCCACNNNTTCATTCNCCNCTANCTCNNAAGTNNNCCNACTCCGNGNNCN
ACCNNCCNNNCCCNCTNGCAGNCNTGTNCNCNNACNNCGGCNACCCNNNGANNNGCNCTCCNCCCGCCCTNT
CNNCACCTNNNNANGGCNTACCNCGCCCTCNGGCTCNGTTACCTTNNNTNNNTNNCCGNCCCNCTCANANNCN
CCNTNACNNGNCNNNCNATNCNTCGCNNNNNAGTANNCCNCNCTCCCCCACNCNCNNNCCGTNTTNNCNCT
TNAGANCT

56C11-1 (5.5X)

modC gene – Same clone as 51A1-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73852

AACGNACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
ACTGACGCGCCCGCAAAAAGGGCGGATTGTCCTCAATGGGCGGGTACTAAATGATGCCGAAAANGGTNTCTTG
CCTGNCCCGTACTANTCGACGCGTGGCCAACNAACCTNCTTNTANNNTCGCNNTTCCCCCTTCNGCNCNTCNN
CCACTCCNGCTGCTCCTNCNNCCTTCCNCGCNCNTACCNTCGTNNCCTTANTCCACCTGCNNCTATCCNCG
GCCCCNCTCCCCGNCCCCCNCTNCAANTNGTTACGNACNGNCCNCCCTCGCCCNAGCGCTNCCNGNGCCAG
NNNCTNTTCATNTCCCTCCNGATCCANTCNCNNCCTTNCNCTCTNACNNNCCNGTCNCTNNCCCCCTNNTTA
N

62C9-2 (20X)

yecK gene (complement) - putative enzyme (cytochrome C type); not classified ,product homologous to
TorC cytochrome of TorCAD resp. system

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74943

CNCGACCGG
GATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACAAAAATCATTAGGGGATTCATCAG
GGTTTCGCTGTCCTTTTGTGCTTGTATGCATTTTCTGCGCAGATTCACTTTGCGAGGCAATATCCATG
GCATCAAAAANAATGGCAACTACGGCACGTTGCAGAGTCAGTGGCTTTTAATTCTTTCCATACTGTTTCG
GCCATTTCTGCGCATGAGCTTCGAACTTATCGTCACTGTCTATTTTGCCGCTAACAAATTCATGATAA
ATATCTTTAGATGC

63E2-3 (2X)

between genes *clpP* and *clpX* – *clpP*: enzyme; degradation of proteins; ATP-dependent proteolytic subunit of *clpA-clpP* serine protease, heat shock protein F21.5. *clpX*: enzyme; degradation of proteins, ATP-dependent component of serine protease, chaperone.

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AAACNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTACCAAAATCATTAGGGGATTCATCAN
GGTTTTGACCCATGACAGATAAACGCAAAGATGGCTCATGCANATTGCTGTATTGCTCTTTTTGCGGCAAAAGC
CNNCATGAAGTGCGCCAGCTGANNAGCCGGNCCATCCCTNTATATCNNCCNNCCCTGTACCTNGNCGGNCNCG
TGGNCNNNCTCCTNTCNTTNNCNTCTCCCNNTCTNNNNCCCCCTCTNNCGCGGNCCCNCCTGANNCGCCTCNCTT
CTTNTACCTCCNCGNGCCTCTACCNCTCGNNCCTCNCCCCCACCTCCTTATTCNCCTCCNTCNTNTCCNTCTC
CACCTNTCCTTTCCNACCGCNCNATNNNACGTCTCNTTCCCTNNNNCCACNNNTNATCCTTCNGCNCNCCCTCNG
NGCGAANCNTCNCTNNNCTANCGGCNCGNTGNNCNTGCNNCNCANTNANCNCNCNCTNATTGAGTGCGNGT

66E10-1 (12X)

ycdS gene (complement) - putative outer membrane protein, same as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CNCGATCCGG
GATATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GTGACGACATCCGTGCCATAATGTTTTTGCCAGGAGGCACCAACACCTGCGCTGAATATTTGCTCCCAGCTATT
TTCATAGCTTCGCCATAACAAATGGCTTGCTCAAATGCCGGAACAATATCNNNCNNNNNGTACTAGTCGAC
GCGTGCCA

68E11-2 (2.5X)

glnE gene (complement) – enzymes, translation and modification; Adenylylating enzyme for glutamine synthetase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000387

Protein Accession # AAC76089

AAACCCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTTATCTGCGTCTGGCGCAACGCATTATGCATCTGTTTCAGTACGCGTACCTCTTCCGGCATTGTA
TGAAGTGGATGCTCGACTGCGTCCGTCCGGGGCGGCGGAATGCTGGTGACATCCGCAGAAGCATTG
CCGATTATCAGAAAAACGAGGCCTGGACGTGGGAACATCAGGCGCTGGTGCGTGCAGTGTAGTGTA
CGGCGATCCGCAGCTCACCGCGCACTTTGACGCAAGTGCCTGCGGAGATTATGACGCTGCCGCGTGAAG
GTAAACTCTGCAACGGAAGTGCGGGAAATGCGCGAGAAATGCGCGCTCATCTCGGCAATAAACA
TCGCGATCGCTTTGATATCAAAGCTGATGAAGGGGAATTACCGATATCGAATTTATTACCCAAT

68A3-1 (>24X)

wcaI gene (complement) - putative enzyme, colanic acid biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_416554

GNCNNCTAAAAACNTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTACCAAAATCATTAGGGGATTCATCAN

GGCCGNNANGGTGTGGCGCTGCCCGCTGTATGTGCCAAAACAGCCGAGCACCCCTGAAACGCCTGTTGC
ATCTGGGCAGTTTTGCCGTCAGCAGTTTCTTTCCGCTGATGGCGCAACGTCGCTGGAAGCCGGATCGCA
TTATTGGCGTGGTGCCAACGCTGTTTTGCGCGCCGGGAATGCGCCTGCTGGCGAAACTCTCTGGTGCGC
GTACCGTGCTGCATATTCAGGATTACGAAGTGGACGCCATGCTGGGGCTGGGCCTTGCCGGAAAAGGC
AAAGGCGGCAAAGTGGCACAGCTGGCAACGG

73E6-6 (16X)

ycdS gene (complement) – putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CGCATCTGGTCTTACCATAATTTGATTGTGCGATTTCTACCCAGTCTGTATTACGAACAAAATACAGAA
CACGATACCCATACTACAACCCTATAAAAACGTTTCGATATNGTCCGGCNGTGTGCTGCNCGNCNNGT
GGNCTGGCGAAGCTATGAAAATAGCTGGGAGCAAATATTACGCGCAGGTGTTGGTGCCTCCTGGCNA
AAACATTATGGCACGGATGTCGTACCCAACTCGGCTACGGGCAACGCATTAGTTGGAATGACGTGAT
TGATGCTGGCGCAACGCTACGCTGGGAAAAACGACCTTATGACGGTGACAGAGAACACAACTTATAC
GTTGAATTCGATATGACATTCAGATTTTAAGGATAAATATGTTACGTAATGGAAATAAATA

73E9-1 (12X)

ycdS gene (complement) - putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

ACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CACCGTACTTACGCCGCTCATTTTTGATACCANCGAACATAAGCCTGAGCACTGTTGCCTGTAACACCATTTTTCA
TTGCCCGTAATGGAACGCGGTGAGAGAGGGCGTTCCAGTTGCGAACCAATACGCCAGTTATCATTAATAATCATAT
CNGCCNGNCCNGTACTAGTCGACGCGTGGCCANAAATTGAAAACCTGGTTTGCCANAATTNTCTNGATCNCCTA
AAAAGCTATNACTGGACNCGNTATNATGGNTNTGNNTTATCTGGNANGGGGNNNCANAAAAATNCGNTGCCA
ATGGNTNATNCAATTGNCCATNAAATTAATAAACATCCCTTANGNTNAAAGACAAATNNATTTTTNTAATTCANG
GGCNA

73F2-1 (12X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NNGNAAACAGCCGGACNTCCCGGATCCGG
GATCATATGACNAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTANGGGATTCATCAG
NCAGATGCGTTCTGACCCTCAAGNGAGACTTCATGACGCTGGTTACTGTGCGGAAAAATCAGTGAAAG
CCCAGGANACACCGTACTTACGCCGCTCATTTTTGATACCAGCGAACATAAGCCTGAGCACTGTTGCCT
GTAACACCATTTTTTATTGCCCCTAATGGAACGCGGTGAGAGAGGGCGTTCCAGTTGCGAACCAATACG
CCAGNTATCATTAATAATCATATCANNCCNGAAGAGGACTAGTCNACGCGTGGCCANNACANCCNCACT
NNTNAACNTGNGGCTACNANTNTACCNGCCANNAGNNTTACNTNANTTNCGCNCNCCTNCCANTCNC
NCCCNANGTNNNCNNAANCTNNANNCTN

75E11-5 (1.5X)

moaC gene - enzyme, biosynthesis of cofactors, carriers: molybdopterin; molybdoproterin biosynthesis, protein C

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000181

Protein Accession # AAC73870

NNAANATACGGTTCGGNTCCG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
ATGGAAGCATTAAACCGCGGCCTCCGTGGCGGCGCTGACCATTTATGACATGTGCAAAGCGGTGCAAAA
AGATATCNCNNCCNNNGTACTAGTCGACGCGTGGCCAAANATCNGGGNTCTCNNNNNTGCTNGCTNC
NAATCNANTGNACCCNCTNAACCCNTTCNAGCTAAACATNTNATNTGNAACNNATAAACNCAGGAC
GNCACTATNGNGTNNACNT

84A10-6 (11X)

ycdR gene - orf, unknown function, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNNGANACGNCCGAATCCG
GATANTANACAAGATGTGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCCGCTTTAA
AAGTCGTGCGTTAACTGACTTCACTTTAGAACTTAGTGCGCGCGTAAAGCCATTCGCGGTCCACATAT
TAAAACTGCACGAAATATTTTGCACCTCCGGTAATACAACCTGAAAGTGAAGCCTGGTTTGCACAGA
ATTATGCTGATTTCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCTGGAAGGTGTCTG
CAGAAAAATCGGCTGACCAATGGTTAATACAATTGA

86E7-6 (10X)

ycdQ gene (complement) - orf, unknown, putative enzyme homologous to IcaA in Staph

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NACGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCGGCGGCATATATTGTGGAACCGAT
GTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTGGTGGG
TAAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATCTATGGAA
ACGTATTTACCGTTT

86F11-6 (11X)

ycdQ gene (complement) - same clone as 86E7-6

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCGGCGGCATATATTGTGGAACCGAT
GTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTGGTGGG
TAAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATCTATGGAA
ACGTATTTACCGTTTCC

91F9-6 (2X)

b2531 gene – orf, function unknown; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC_000913

Protein Accession # NP_417026

CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACAAAATCATTAGGGGATTCATCAN
GGGCCCCGGTACCGTTGGCTGATATTTCCGAACGTACAGGAATTTCCCTTTCTTATCTGGAACAACCTGTTTTCCCG
TCTGCGTAAAAATGGTCTGGTTTCCAGCGTACGTGGACCAGGCGGTGGTTATCTGTTAGGCAAAGATGCCAGCA
GCATCGCCGTTGGCGAAGTAATTAGCGCCGTTGACGAATCTGTAGATGCCACCCGTTGTCAGGGTAAAGGCGG
CTGCCAGGGCGGCGATAAATGCCTGACCCACGCGCTGTGGCGTGATTTGAGCGACCGTCTCACC GGTTTTCTCA
ACAACATTACTT

93E3-6 (12X)

ycdR gene (complement)– orf, function unknown; product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACAAAATCATTAGGGGATTCATCAG
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCCGCTTTAA
AAGTCGTGCGTTAACTGACTTCACTTTAGAACTTAGTGCGCGCGTAAAAGCCATTCGCGGTCCACATAT
TAAAACTGCACGAAATATTTTTGCACCTCCGGTAATACAACCTGAAAAGTGAAGCCTGGTTTGCACAGA
ATTATGCTGATTTCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCTGGAAGGTGTGCG
CAGAAAAATCGGCTGACCAATGGTTAATACAATTGACCAATCAAATTA AAAACATCCCTCAGGCTAAA
GACAAATCTATTTTAGAATTACAGGC

96B10-1 (11X)

nhaR - regulator, transport of sm molecules - cations; encodes a positive regulator for nhaA(a Na/H antiporter)
stimulates transcription of osm-c

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000112

Protein Accession # AAC73131

NCAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTTACAAAATCATTAGGGGATTCATCAG
GTTTATGCTGACTTAATTGCTCCAGCAGCATTTCTGTGGGTGGATTCTGAAGCAGCGAAGATGAATGGGC
TCGCCTTCTACCACTGCGGCGTTAAGTACGCTACTGACCAGGCGTTTGGAAAAGTGCATCAGCCACGCC
AACGTCAAACAATAAATTGGATTCTTTGCGATAGTTCACAATATCCNNC NNNNCCGTACTAGTCGACG
CGTGGCCAN

102G9-5 (5X)

leuO gene – Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAACNCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACAAAATCATTAGGGGATTCATCAG

AGTTAAGTGTGACAAAGTGGAGTTAAGTATGCCANAGGTACAAACAGATCATNCAGAGACGGNGGAGT
TAAGCAAACCACAGCTACAGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAGGA
NCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCNNNGCNGNACTAGTTCGACGCGTGG
CCNCATANNATGTNTCANNNTTNNNNCTCTTCNNTTGCTTCCCTTNNCCCTCTTCCNGCCCCCANNNC
GTCTNNTNTNATCANNNGNNCTTNNCNTACGACTN

106B2-6 (5X)

leuO gene – same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

AAACCCNTNGGATCCNG
CATCATATGACAAGANGTTGTATCCACCTTAACCTTAATGATTNTTACCAAANTCATTAGGGGATTCATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGTGGAGTTAAGCAA
ACCACAGCTACNGCATGGTCGATCTCAACTTNTTAACCGTTTTCGATGCCGTGATGCAGGAGCAAAACATTACT
NCGTGCCGNTCATGTTCTGGGAATATCCCNNGGNNACGTNCTAGTCNANGCGTGGCCAANNNGTNNGGNNCT
NANTCACAGNANCTTTANNNGTN

109B4-4 (2X)

Between two protein binding sites (complement) - 1)central position to predicted promoter: -0.5/LexA predicted site and 2)documented lrp site/ central position to leuABCD promoter:- 156.5

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AGCNCGCCGACNTCCCGGATCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTNTTACCAAATCATTAGGGGATTCATCAG
TCGGTAGTTAAGCAGAAATTAATATCGCTTACTTTAACCACCGCAGCACAATTAGCTAATTTTACGGAT
GCAGAACTCACGCTGGCGGGACGTTTTTATTGCGTCAGGGTTGACATCCGTTTTTGTATCCAGTAACTC
TAAAAGCATATCGCCCCCNCNGTACTAGTCGACGCGTGGCCANAACNCGNNNTCCANTNTNNCC

110G8-2 (9X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

GNAANGNAAAACNCGCCGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTNTTACCAAATCATTAGGGGATTCATCAG
NACNGCNNATTGNNCCCAACGGNGGANTAANTNGCCCCNGNTTGNNTTCTCGCTGNTAANGANAAATA
ACGTCTTTATAACGANCGCGAGTNAATAACGCGCCAAGATGATCAACCTGAATACNCTGGTACTGGGC
AGTGCGGTCTGGGTTATCGTGCCACAGAATTTCTAATGCAGCGTATTGGGCGAGGGCGCGATCGGCAA
TGGCATAACGNTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTTCGGCATGAATATCA
GNNNTTGNTGNACTAGNCNACGCGTGGNCAAAACAT

115C12-5 (16X)

ycdR gene (complement) – orf unknown function; product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGCTTAATACCGGCATCCACGCATAGATGTTTACACCTGAGCGGGTACGTAATTGCCAGGCAACCCGA
CTAAAAATATCTGCTTTTCATTGGNCTNANACAANCNGGANCCAGACCTCTTTGACCAGCCCATCACC
ATCGGGATCAGCAAATGCCTGCAAATACACGGTTGATATTTGCATATCTTTCCCCNCGTAAGTCTCGA
CGCGTGGCCACATTACTTNTANTNTANNANTGGATCCNANTNANNCGGNTNTANCTNGCCTTGNANGG
GNGNNANNATTATCENNCTGCCNCCGACNAANT

123F5-6 (4X)

modA gene - transport, small molecules: anions; molybdate-binding periplasmic protein; permease

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73850

TTTNGAAACACGCCGNACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGGATTATGCGGTTGATAAAAAAGCGATCGATACAGCTACGCGTCAGACACTGCTCGGCAATAGCCTG
GTCGTTGTAGCACCAGAAAGCCAGCGTGCAGAAAGATTTACCATCGACAGCAAAACCAACTGGACTTC
ACTGCTGAATGGCGGTCGCTGGCGGTTGGCGATCCGGAACATGTTCCCGCTGGCATTATGCAAAAG
AAGCACTGCNAAAACCTGGGCGCATGGGATACNCTCNCTCCGAAAATGGNCCNCNTAAGNTGNTCCT
AGGGGNNCNCNCGCNGGTACCAACNTAATCGAACC

125A7-1 (2.5X)

rbsK gene - enzyme, degradation of small molecules: carbon compounds; ribokinase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000452

Protein Accession # AAC76775

GCAAAAACGANNCGGCCAAG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GAAAGGGCAGCNTTANCGCCGGCATGAATACCGATGACATTCTACCTTCGCCATTAACAAAAATCAN
CGCCACACCTGTTGATTGCTCTTGTATCTCGCTGACCGGAGTAANATCCCCNTNNNNGNACTAGTCNA
CGCGTGGCCATNAANTTCNNNCGACCNANTANGACCCNANTCCTGNNNTTAANNCCNCGNNTNCCNTANTT
GCNCCANNN

125E4-1 (24X)

insB_4/insA_3/insA_2 genes (complement) - all three have the same probability score and identities,89% -
IS,phage,Tn; transposon-related function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

CACANCCGNACATCNGCGNT
ATNNCTACTNANAATGNCGTGAANTATTCNCACTGCNTNACACTTACACCGNNTCTCATNCCGGTANGC
ACCACANAAANNNTGAATATGAGGCATGAATGGTNGTTGGANGCCGGGTAACAGCCNTCATTATGGG
NGTTGGCCTCAACACGATTTTCTCCNTTTAAAAAACTCACGCCGNTACCCTGTAACTCGCACCATAC
TGGCAGGGCAGCNGACNGATTGCGCTGCGCATGAAATGNANAAACNNTGGGGATNACCAGGGNGTA
AATCTNGCCAGCGATNNCTGNNTTNTCTNTGANANGATNCNGAAAANGGGGGNTGCNCNCGTNTN
CCGGNAAACATCNNTAATAAACTGGGGCCAAAGTAAACGTGCGGATATCCAATCCANNNGTACTA
NTCGACGCGTGGCCANNACTGNC

126C5-4 (7.5X)

leuO gene - same clone as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

NNACGCTNCGGNNCCG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAGTT
AAGCAAACACAGTCTACGCATGGTCGATCTCAACTATTAACCGTTTTTCGATGCCGTGATGCAGGAGC
AAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCCCCNCTNNGTACTAGTCGACGCGTGGCCA
NN

130E8-4 (24X)

Between yecK and cutC genes (complement) - in a protein binding area with no predicted promoter; TyrR predicted site

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

ATNCNCGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAN
NGTCCAGTAATTCAATTANAGGAATCTATGCGNGGGANAAACGGNTGGCNGCTNCNCGCTAANGCNA
ANAANTAANCCNCTNNNNCTANGTATNNNNGGGNCNNTNNNANNNCNGNTTTCT

130G11(2.5X)

aroD gene – enzyme: amino acid biosynthesis: chorismate; 3-dehydroquinase dehydratase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000264
Protein Accession # AAC74763

ANNCNCGACCGG
GNTCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TCNGGCCGANCNGGCNATTTCCACCGAGGCTTATNTCCNCCNNTNTCGNNTAGNCGNNGCNTGGCCA
NGNTTNCGNCCNNTNACNCTCCATNANTNTNCCNCTNTCNCNNTACNGTGCCCGNGNATNC
CCNTCCTCCGTGCGCCCCCNCNNGCTTAGCNGCANNANTGGCCNNNNNNCAANTTANGACGATCNGCC
NGCCCNNTNAAACNGNGTTNGCCATNTNCTNCTNTTATN

140B5-1 (9X)

miaA gene – enzyme, Aminoacyl tRNA synthetases, tRNA modification; delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000489
Protein Accession # AAC77128

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGGCAAGTCCGTATGCAAATCTCCTCGGGCAAAAAGCGCCCGGACTTCTGCTTCAAAACCTGAAGCCA
ACATCTGATGAAAACGCTGCTCAATGCGTTGATGGAGCAGTTCACGGCTCGCCGGGGCGATGGCGAAC
TGATGCACCTGATACGGTAGAGCGTCTCCTGACGTTTGCCTCAGTTCGTTAAAGTTTTACCCGAAATG
AAAAAACTTCCAGTGCCCGGAAAGCCTTTGTGGATCATTTGGATGAATCCTTGCTGCCGCAACCGG
ATCTACCTCCTGAAGTTGACGATGCAATGACTCCCAACCTTGCTCTGCCGCTGTTGCTCAATTCTGGC
CCGTACTTCCGGGTCTGCCGACGGTAGCGGCGACAACCCTTCCAGCAATGCCTTGAAAT

141G2-2 (16X)

yjjQ gene - putative regulator, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000507
Protein Accession # AAC77321

GNCGGATCCGG
TATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGGGGCATCAACCAGATAGCTTTCATTGCTTAAGAAAAAGTAATAAACTATCANCGCCCAAAAAA
CAGTGGCATGCGTCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGCGCAG
GGTGCAAGAGAAGCTTAACCTGCCTTCTGTTTATGGAGATGCCGCAGAATGGAACACAGCCGAATTAAG
AAGAGAAATGTCGCACTC

141G4-6 (18X)

ycdS gene (complement) - putative outer membrane protein; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

NNNAAAGCACGCCGGACATCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ACCCAATATTGCCCCAGGGCGGAATAATTTGCCCCGCTTTTTTAATCGCTGATAGTGAGAAATAACG
TCTTTATAACGATCGCGAGTTATAACGCGCCAAGATGATCAACCTGAATACGCTGGTACTGGGCAGTG
CGGTCTGGGTTATCGTGCCACAGAATTTCTAATGCAGCGTATTGGGCGAGGGCGCGATCGGCAATGGC
ATAACGTTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTCGGCATGAATATCANC
GAATAGTACTAGTCGAC

145F10 (3X)

ykgK gene (complement) - putative regulator; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000136
Protein Accession # AAC73397

NNNNGAAGCNCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TACCACGCCCCCTAATATTGCTATTGTAATACCAATAATTTGCTAAGGCCCTGACTTTCTGGCCGCAAT
CAATACGACCTGTTTCCCTTTACCGCGGATAACCATTCATTATCACGGTTTATAAATTCAGATAAAGA
ATCCGTAAGTATGATAAACACGAAATCTTTTCTAATTTTCTCCAACGATAGATAAATTAATCTGTC
GATATCCCCCNNCNNNGTACTAGTCGACGCGTGGCCA

150E3-6 (20X)

ycdP gene (complement) - orf, hypothetical protein unknown function

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_000913
Protein Accession # NP_415540

NACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCCAGAAGCCGACTTCAGTTCTATTTTTGCTGGCAGTGGCGAATGCCGTCGTGTTAATTGTCTGGGCGCTGT
ACAATAAGCTGCGTTTTCAAAAACAGCAGCATCATGCAGCCTACCAATATACGCCGCAAGAATATGCAGAGAG
CTTAGCAATACCTGATGAGCTCTATCAGCAACTACAAAAAGCCACAGGATGAGCGTACACTTCACCAGCCAG
GGGCAAATAAAAAATGGTTGTTTCAGAAAAAGCGCTAGTCCGGGCATAAACACCCAAAAACAAAGCCCGGTTTCG
CCGGGCTCTGCACCGATAACACACTTAACCTGTAGGCATGCAGCGTACGTTGGCAAAGTGCCGAACGTACGCAN
T

150G7-2 (4X)

prfC gene- Factor; protein translation and modification; peptide chain release factor RF-3.

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000508

Protein Accession # AAC77328

ANACNCGTCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTANGGGATTTCATCAG
TGTGGTGTCCGGTAAATATGAAAAAGGCATNAAACTGCNCCACGAGCCCACTGCNAANGATGNGGNA
ATCTCCGCCCGCNGCCTCTCTGGCNGGTNNCCGTTCTCACCTTNNACACCNCCCCNNGCTCNCNTNCN
CTCCCNACNNCNCNTTCTCTCNGCANCCCACTTNACTNCCNCCCTCCCNACGNNTCCCNCCCC
NCNGNNCNANTGNNTTGGCTNNCGNCCNNNANNCNCNCTCCTGGCCTCNCNTTACNCNN

155F4-4 (20X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

NNCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
CACTTGTTGCCACGTGGCAAAATATTCTCGATCGACCAACTCATCGCCAAATTTTACTTGTTTATCCGG
TGGCATATCNCNNCCNNNCGTACTAGTCGACGCGTGGCCANN

160A8-6 (20X)

yjjQ gene - putative regulator; not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000507

Protein Accession # AAC77321

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
GGCATCAACCAGATAGCTTCATTGCTTAAGAAAAGTAATAAACTATCAGCGCCCCAAAAAACAGTG
CGATGCGTCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGCGCAGGGTGC
AAGAGAACTTAACCTGCTTCTGTTTATGGAGATGCCGCAGAATGGAACACAGCCGAATTAAGAAGAG
AAATGTCGCACTCATAGAAAAATGCGTCATGAGTAGTATCGGTATTGAGAGTTTATTCAGAAAGTTTG
CGGGTAACCCTTATAAGCTCCATACCTATACCAGTCAGGAGTCATTCAGGATGCCATGTCGCGGATA
TCCNCCNCCNCGTACTAGTCGACGCGTGGCCAA

169G4-6 (18X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

AAAANCNCGCCGGACATCCCGGATCCGGGATCAT
ATGACAAGGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTTCATCAG
TATTAATCGCCAATAATCCCTCATTAAGAGTTTGCCAGCAAATTATTACCGTACAGGAAAAATCA
CCACAACGGATAATGCATATCNCNCCNNNNNGTACTAGTCGACGCGTGGCCACANAN